

This figure displays a sequence alignment of PKA catalytic subunits (PKACα) from various species. The alignment is color-coded to highlight conservation of amino acid residues. The x-axis represents the amino acid position, ranging from approximately 400 to 600. The y-axis lists the species and their corresponding genes:

- 113r\_PKACα**
- 1jlu\_AMPK**
- 31213155.i**
- 24667016.f**
- 27370078.m**
- NDR2.h**
- 34852268.m**
- 19527344.m**
- NDR1.h**
- 32566202.w**
- 15234064.p**
- 27420006**
- 18399030.p**
- AK101120**
- 55960009**
- 30682086.p**
- 30682811.p**
- 22331282.p**
- 15225358.p**
- 15219591.p**
- 16418172**
- 15221465.p**
- 18416116.p**
- 1muo\_AUR1**
- 1omw\_GPRK2**

The alignment shows high conservation of the kinase domain, particularly the ATP-binding site and the catalytic loop. The N-terminal region and C-terminal tail show more variability. The color scheme used for conservation includes:

- Red: Conserved in all species.
- Green: Conserved in most species.
- Blue: Conserved in some species.
- Cyan: Conserved in a few species.
- Magenta: Conserved in a single species.

The figure displays a sequence alignment of GPRK2 orthologs from various species. The alignment is color-coded to highlight conservation: red for highly conserved residues, green for moderately conserved, blue for less conserved, and grey for non-conserved or missing residues. The alignment includes the following species and their corresponding protein names:

- 113r\_PKA<sub>c</sub>**
- 1jlu\_AMPK**
- 31213155.i**
- 24667016.f**
- 27370078.m**
- NDR2.h**
- 34852268.m**
- 19527344.m**
- NDR1.h**
- 32566202.w**
- 15234064.p**
- 27420006**
- 18399030.p**
- AK101120**
- 55960009**
- 30682806.p**
- 30682811.p**
- 22331282.p**
- 15225358.p**
- 15219591.p**
- 16418171.p**
- 15221465.p**
- 18416116.p**
- 1muo\_AUR1**
- 1omw\_GPRK2**

Key features of the alignment include:

- Conservation:** The alignment shows high conservation of the kinase domain, particularly the ATP-binding site (around positions 600-700) and the activation loop (around positions 350-450).
- Mutations:** Several mutations are highlighted, such as the 'Q' to 'R' mutation at position 113 in the NDR2.h ortholog.
- Color Coding:** The color scheme (red, green, blue, grey) provides a visual summary of the evolutionary conservation of each amino acid position across the different orthologs.